

OIIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/955,866

DATE: 10/09/2001

TIME: 09:30:19

Input Set : A:\00759Aseq.txt

Output Set: N:\CRF3\10092001\I955866.raw

2

ENTERED

p. 5

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3 <110> APPLICANT: Fox, Michael
4 Sullivan, John K.
5 Holst, Paige
6 Yoshinaga, Steven Kiyoshi
8 <120> TITLE OF INVENTION: B7-Like Polypeptides and Uses Thereof
10 <130> FILE REFERENCE: 00,759-A
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/955,866
C--> 13 <141> CURRENT FILING DATE: 2001-09-19
15 <150> PRIOR APPLICATION NUMBER: 60/233,867
16 <151> PRIOR FILING DATE: 2000-09-20
18 <160> NUMBER OF SEQ ID NOS: 30
20 <170> SOFTWARE: PatentIn Ver. 2.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1209
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
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28 <221> NAME/KEY: CDS
29 <222> LOCATION: (33)..(854)
31 <220> FEATURE:
32 <221> NAME/KEY: sig_peptide
33 <222> LOCATION: (33)..(89)
35 <220> FEATURE:
36 <221> NAME/KEY: misc_feature
37 <222> LOCATION: (693)..(755)
38 <223> OTHER INFORMATION: predicted transmembrane domain
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41 cagaaagaga cctatatgat caaatacaga ac atg atc ttc ctc ctg cta atg 53
42 Met Ile Phe Leu Leu Leu Met
43 1 5
45 ttg agc ctg gaa ttg cag ctt cac cag ata gca gct tta ttc aca gtg 101
46 Leu Ser Leu Glu Leu Gln Leu His Gln Ile Ala Ala Leu Phe Thr Val
47 10 15 20
49 aca gtc cct aag gaa ctg tac ata ata gag cat ggc agc aat gtg acc 149
50 Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu His Gly Ser Asn Val Thr
51 25 30 35
53 ctg gaa tgc aac ttt gac act gga agt cat gtg aac ctt gga gca ata 197
54 Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn Leu Gly Ala Ile
55 40 45 50 55
57 aca gcc agt ttg caa aag gtg gaa aat gat aca tcc cca cac cgt gaa 245
58 Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser Pro His Arg Glu
59 60 65 70
61 aga gcc act ttg ctg gag gag cag ctg ccc cta ggg aag gcc tcg ttc 293
62 Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly Lys Ala Ser Phe
63 75 80 85
65 cac ata cct caa gtc caa gtg agg gac gaa gga cag tac caa tgc ata 341
66 His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln Tyr Gln Cys Ile

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67          90          95          100
69 atc atc tat ggg gtc gcc tgg gac tac aag tac ctg act ctg aaa gtc 389
70 Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu Thr Leu Lys Val
71          105          110          115
73 aaa gct tcc tac agg aaa ata aac act cac atc cta aag gtt cca gaa 437
74 Lys Ala Ser Tyr Arg Lys Ile Asn Thr His Ile Leu Lys Val Pro Glu
75 120          125          130          135
77 aca gat gag gta gag ctc acc tgc cag gct aca ggt tat cct ctg gca 485
78 Thr Asp Glu Val Glu Leu Thr Cys Gln Ala Thr Gly Tyr Pro Leu Ala
79          140          145          150
81 gaa gta tcc tgg coa aac gtc agc gtt cct gcc aac acc agc cac tcc 533
82 Glu Val Ser Trp Pro Asn Val Ser Val Pro Ala Asn Thr Ser His Ser
83          155          160          165
85 agg acc cct gaa ggc ctc tac cag gtc acc agt gtt ctg cgc cta aag 581
86 Arg Thr Pro Glu Gly Leu Tyr Gln Val Thr Ser Val Leu Arg Leu Lys
87          170          175          180
89 cca ccc cct ggc aga aac ttc agc tgt gtg ttc tgg aat act cac gtg 629
90 Pro Pro Pro Gly Arg Asn Phe Ser Cys Val Phe Trp Asn Thr His Val
91          185          190          195
93 agg gaa ctt act ttg gcc agc att gac ctt caa agt cag atg gaa ccc 677
94 Arg Glu Leu Thr Leu Ala Ser Ile Asp Leu Gln Ser Gln Met Glu Pro
95 200          205          210          215
97 agg acc cat cca act tgg ctg ctt cac att ttc atc ccc tcc tgc atc 725
98 Arg Thr His Pro Thr Trp Leu Leu His Ile Phe Ile Pro Ser Cys Ile
99          220          225          230
101 att gct ttc att ttc ata gcc aca gtg ata gcc cta aga aaa caa ctc 773
102 Ile Ala Phe Ile Phe Ile Ala Thr Val Ile Ala Leu Arg Lys Gln Leu
103          235          240          245
105 tgt caa aag ctg tat tct tca aaa gac aca aca aaa aga cct gtc acc 821
106 Cys Gln Lys Leu Tyr Ser Ser Lys Asp Thr Thr Lys Arg Pro Val Thr
107          250          255          260
109 aca aca aag agg gaa gtg aac agt gct atc tga acctgtggctc ttgggagcca 874
110 Thr Thr Lys Arg Glu Val Asn Ser Ala Ile
111          265          270
113 ggggtgacctg atatgacatc taaagaagct tctggactct gaacaaagaat tcggtggcct 934
115 gcagagcttg ccatttgcac ttttcaaatg cctttggatg acccagcaact ttaactgaa 994
117 acctgcaaca agactagcca acacctggcc atgaaacttg ccccttcaact gatctggact 1054
119 cacctctgga gcctattggct ttaagcaagc actactgcac ttacagaaat taccccaactg 1114
121 gatcctggac ccacagaatt ccttcaggat ccttcttgct gccagactga aagcaaaaag 1174
123 aattatttcc cctcaagttt tctaagtgat ttcca 1209
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127 <211> LENGTH: 273
128 <212> TYPE: PRT
129 <213> ORGANISM: Homo sapiens
131 <400> SEQUENCE: 2
132 Met Ile Phe Leu Leu Leu Met Leu Ser Leu Glu Leu Gln Leu His Gln
133 1 5 10 15
135 Ile Ala Ala Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile
136 20 25 30

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Input Set : A:\00759Aseq.txt
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138 Glu His Gly Ser Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser
139      35      40      45
141 His Val Asn Leu Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn
142      50      55      60
144 Asp Thr Ser Pro His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu
145      65      70      75      80
147 Pro Leu Gly Lys Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp
148      85      90      95
150 Glu Gly Gln Tyr Gln Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr
151      100      105      110
153 Lys Tyr Leu Thr Leu Lys Val Lys Ala Ser Tyr Arg Lys Ile Asn Thr
154      115      120      125
156 His Ile Leu Lys Val Pro Glu Thr Asp Glu Val Glu Leu Thr Cys Gln
157      130      135      140
159 Ala Thr Gly Tyr Pro Leu Ala Glu Val Ser Trp Pro Asn Val Ser Val
160      145      150      155      160
162 Pro Ala Asn Thr Ser His Ser Arg Thr Pro Glu Gly Leu Tyr Gln Val
163      165      170      175
165 Thr Ser Val Leu Arg Leu Lys Pro Pro Gly Arg Asn Phe Ser Cys
166      180      185      190
168 Val Phe Trp Asn Thr His Val Arg Glu Leu Thr Leu Ala Ser Ile Asp
169      195      200      205
171 Leu Gln Ser Gln Met Glu Pro Arg Thr His Pro Thr Trp Leu Leu His
172      210      215      220
174 Ile Phe Ile Pro Ser Cys Ile Ile Ala Phe Ile Phe Ile Ala Thr Val
175      225      230      235      240
177 Ile Ala Leu Arg Lys Gln Leu Cys Gln Lys Leu Tyr Ser Ser Lys Asp
178      245      250      255
180 Thr Thr Lys Arg Pro Val Thr Thr Thr Lys Arg Glu Val Asn Ser Ala
181      260      265      270
183 Ile
186 <210> SEQ ID NO: 3
187 <211> LENGTH: 254
188 <212> TYPE: PRT
189 <213> ORGANISM: Homo sapiens
191 <220> FEATURE:
192 <221> NAME/KEY: TRANSMEM
193 <222> LOCATION: (202)..(222)
195 <400> SEQUENCE: 3
196 Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu His Gly
197      1      5      10      15
199 Ser Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn
200      20      25      30
202 Leu Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser
203      35      40      45
205 Pro His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly
206      50      55      60
208 Lys Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
209      65      70      75      80

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211 Tyr Gln Cys Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
212                85                90                95
214 Thr Leu Lys Val Lys Ala Ser Tyr Arg Lys Ile Asn Thr His Ile Leu
215                100                105                110
217 Lys Val Pro Glu Thr Asp Glu Val Glu Leu Thr Cys Gln Ala Thr Gly
218                115                120                125
220 Tyr Pro Leu Ala Glu Val Ser Trp Pro Asn Val Ser Val Pro Ala Asn
221                130                135                140
223 Thr Ser His Ser Arg Thr Pro Glu Gly Leu Tyr Gln Val Thr Ser Val
224 145                150                155                160
226 Leu Arg Leu Lys Pro Pro Gly Arg Asn Phe Ser Cys Val Phe Trp
227                165                170                175
229 Asn Thr His Val Arg Glu Leu Thr Leu Ala Ser Ile Asp Leu Gln Ser
230                180                185                190
232 Gln Met Glu Pro Arg Thr His Pro Thr Trp Leu Leu His Ile Phe Ile
233                195                200                205
235 Pro Ser Cys Ile Ile Ala Phe Ile Phe Ile Ala Thr Val Ile Ala Leu
236                210                215                220
238 Arg Lys Gln Leu Cys Gln Lys Leu Tyr Ser Ser Lys Asp Thr Thr Lys
239 225                230                235                240
241 Arg Pro Val Thr Thr Thr Lys Arg Glu Val Asn Ser Ala Ile
242                245                250
245 <210> SEQ ID NO: 4
246 <211> LENGTH: 224
247 <212> TYPE: PRT
248 <213> ORGANISM: Homo sapiens
250 <400> SEQUENCE: 4
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252 1                5                10                15
254 Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
255                20                25                30
257 Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
258                35                40                45
260 Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
261                50                55                60
263 Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
264 65                70                75                80
266 Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
267                85                90                95
269 Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
270                100                105                110
272 Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
273                115                120                125
275 Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
276                130                135                140
278 Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
279 145                150                155                160
281 Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
282                165                170                175

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284 Glu Asn Gly  Glu  Glu  Leu  Asn  Ala  Ile  Asn  Thr  Thr  Val  Ser  Glu  Asp
285              180              185              190
287 Pro Glu Thr  Glu  Leu  Tyr  Ala  Val  Ser  Ser  Lys  Leu  Asp  Phe  Asn  Met
288              195              200              205
290 Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
291      210              215              220
297 <210> SEQ ID NO: 5
298 <211> LENGTH: 323
299 <212> TYPE: PRT
300 <213> ORGANISM: Homo sapiens
302 <400> SEQUENCE: 5
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304      1              5              10              15
306 Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu
307              20              25              30
309 Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val
310              35              40              45
312 Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu
313      50              55              60
315 Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr
316      65              70              75              80
318 Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile
319              85              90              95
321 Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr
322      100              105              110
324 Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala
325      115              120              125
327 Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn
328      130              135              140
330 Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro
331      145              150              155              160
333 Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Ser Thr Ile Glu Tyr
334              165              170              175
336 Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp
337              180              185              190
339 Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met
340              195              200              205
342 Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser
343      210              215              220
345 Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Ile
346      225              230              235              240
348 Pro Trp Ile Thr Ala Val Leu Pro Thr Val Ile Ile Cys Val Met Val
349              245              250              255
351 Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys Lys Arg Pro Arg Asn
352      260              265              270
354 Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu Ser Glu Gln
355      275              280              285
357 Thr Lys Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser Asp Glu Ala
358      290              295              300

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\00759Aseq.txt

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L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:548 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1086 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1088 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1090 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1148 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1154 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
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L:1158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
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L:1162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
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L:1174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1180 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1182 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1188 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
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L:1194 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1286 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
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L:1320 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
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L:1324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
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L:1328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1338 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16

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L:1488 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16

L:1492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16

L:1494 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16

L:1496 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16